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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=6; hr=8; min=54; sec=0; ms=423;]

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Reviewer Comments:

<210> 5
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<223> Xaa = Asn, His, Gln, Cys, Ser, Thr

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<223> Xaa = any amino acid residue

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20 25 30

Xaa Xaa Leu Leu Arg Xaa His Xaa Xaa Leu Xaa Xaa Ala Xaa Xaa Arg

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Ser Leu Val Xaa Xaa Xaa Xaa Xaa Leu

50 55 60

Lys Xaa Xaa Ala Tyr Asp Ala Xaa Asp Xaa Leu Xaa Glu Xaa Glu Xaa

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Xaa Ala Xaa Xaa Xaa Lys Val

85

The "<213> Artificial Sequence" needs explanation in a <220>-<223> section; please give the source of the genetic material. Same error in Sequences 6-7.

Application No: 10573372 Version No: 3.0

Input Set:

Output Set:

Started: 2009-05-05 15:29:03.484
Finished: 2009-05-05 15:29:15.521
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 37 ms
Total Warnings: 3
Total Errors: 3
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

Error code	Error Description
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SEQUENCE LISTING

<110> Dale, James Langham
Echeverria, Santy Peraza

<120> BANANA RESISTANCE GENES AND USES THEREOF

<130> DAVI172.006APC

<140> 10573372

<141> 2009-05-05

<150> PCT/AU2004/001300

<151> 2004-09-23

<150> AU 2003905222

<151> 2003-09-25

<160> 7

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49

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Gln Thr Leu Leu Asp Lys Ala Ser Asn Cys Ala Ile Gln Gln Leu Ala
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5560

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Lys Asn Thr Ser Leu Val Glu Leu Val Arg Gln Leu Lys Asp Ala Ala
65 70 75 80

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100	105	110	
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Ser Leu Ser Thr Ala Ser Glu Trp Leu Gly Ala Asp Gly Asp Asp Ala			
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165	170	175	
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Glu Thr Val Val Phe Gly Arg Asp Gln Glu Arg Glu Lys Val Val Glu			
180	185	190	
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Lys Thr Leu Gly Ser Leu Leu Arg Leu Asp Val Ser Gln Glu His Trp				
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Arg Thr Ile Met Glu Ser Glu Val Trp Gln Leu Pro Gln Ala Glu Asn				
405	410	415		
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Glu Ile Leu Pro Val Leu Trp Leu Ser Tyr Gln His Leu Pro Gly His				
420	425	430		
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435	440	445		
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Phe Tyr Lys His Glu Leu Ile Gln Thr Trp Ile Ala Glu Gly Phe Ile				
450	455	460		
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Ala His Gln Gly Asn Lys Arg Met Glu Asp Val Gly Ser Ser Tyr Phe				
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485	490	495		
cga tat gtg atg cat gac ctc ata cac gat ctt gcc caa ttt ata tca				1536
Arg Tyr Val Met His Asp Leu Ile His Asp Leu Ala Gln Phe Ile Ser				
500	505	510		
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Val Gly Glu Cys His Arg Ile Asp Asp Asp Lys Ser Lys Glu Thr Pro				
515	520	525		
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Ser Thr Thr Arg His Leu Ser Val Ala Leu Thr Glu Gln Met Lys Leu				
530	535	540		

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cct cat agc ttg ttc aaa aga ctg aaa aga atc cat gtt tta gtt ttg Pro His Ser Leu Phe Lys Arg Leu Lys Arg Ile His Val Leu Val Leu	580	585	590		1776
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ccc gag tca ttg tgc gac ctt tac aat ctg caa gca ctg agg cta tgg Pro Glu Ser Leu Cys Asp Leu Tyr Asn Leu Gln Ala Leu Arg Leu Trp	625	630	635	640	1920
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gtt ggg aag ctg att tct ctg caa gaa ttg tct gca ttc aaa gtg cta Val Gly Lys Leu Ile Ser Leu Gln Glu Leu Ser Ala Phe Lys Val Leu	675	680	685		2064
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785	790	795	800
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aag gtc ctt cat atg aag aga atg cct gtg gtg aaa caa atg agt cat			2496
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Asn Met Ser Ala Leu Lys Leu Ile Gly Arg Glu Leu Cys Asp Ser Arg			
930	935	940	
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980	985	990	
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1190	1195	1200	
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1205

1210

1215

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